

REMARKS

Status of the Claims

Claims 1-97 were pending. Claims 1-37, 40-44 and 46-97 were withdrawn pursuant to a Restriction Requirement that has been made FINAL and is discussed below. Claims 2, 3, 4 and 38 have been amended as shown above to make explicit that the polynucleotide of the expression cassettes exhibits at least 90% identity to the full-length of the sequence identified in the claim. Claims 78 and 91 have been amended to depend from examined claim 38. Claims 1, 5-37, 39-77 and 97 have been canceled without prejudice or disclaimer. Thus, claims 2-4, 38 and 78-96 are pending of which claim 38 has been examined.

Restriction Requirement

As noted above, the Restriction Requirement has been made FINAL. In this regard, the Examiner asserts that § 803.04 of the MPEP indicating that 10 sequences should be examined together is "only a guideline and not legally binding" and that this application is not eligible for this option because it is not a SPDI application. (Office Action, page 1).

As correctly noted by the Office, it is well settled that two criteria must be met for a proper restriction requirement under M.P.E.P. § 803: (1) the inventions must be independent or distinct as claimed; and (2) there must be a serious burden on the Examiner if restriction is not required. However, Applicants respectfully submit that the Examiner has not met this burden.

Here, given the high homology between the sequences, the Examiner cannot show that it would impart a serious burden to examine the sequences together. Indeed, the Examiner has not even shown that the nucleotide sequence encode "structurally different envelope glycoproteins" as asserted on page 2 of the Office Action. In fact, the sequences exhibit high homology to each other and a search of the art for sequences relevant to any of SEQ ID NOs:46, 47, 49, 97, 119, 120, 121, 122, 123, 124, 125, 126, 127, 131, 132, or 133 would necessarily reveal art relevant to the other sequences.

In this regard, Applicants again direct attention to the alignment of SEQ ID NOs:120 and 121 submitted with the Response to Restriction Requirement and submitted herewith again for the Examiner's convenience. In addition, Applicants attach hereto an alignment of all of the sequences recited in claim 38 along with SEQ ID NOs: 46 and 47 (claims 2 and 3, depicting common regions of Env). All of these sequences exhibit high homology to each other.

In view of the high degree of homology between the sequences of all the pending claims, it is clear that searching the art for the full-length of any of these sequences would necessarily reveal references relevant to all other sequences and, as such, it would not impart a serious burden on the Examiner to search them together. By contrast, it would certainly impart a serious financial burden

on Applicants to file individual applications to each highly-related sequence. No serious burden on the Examiner coupled with a very serious burden on Applicants does not meet the goal of Restriction practice.

Accordingly, Applicants again submit that the Restriction Requirement as between pending claims 2, 3, 4 and the individual sequences of claim 38 cannot stand because the two criteria of M.P.E.P. § 803 have not been fulfilled.

Thus, Applicants reiterate that claims 2-4 should be examined with claim 38. Furthermore, Applicants request rejoinder of process claims 78-96 when the elected product claims are found allowable.

Finally, Applicants expressly reserve their right under 35 USC §121 to file one or more divisional applications directed to the nonelected subject matter during the pendency of this application.

Sequence Listing

As the objection to the Sequence Listing was not reiterated, Applicants conclude that the Sequence Listing and accompanying computer readable form accompanying the Preliminary Amendment as filed on May 29, 2003 is acceptable.

IDS

The Examiner has requested, seemingly pursuant to 37 C.F.R. § 1.98(a)(3)(i), a statement identifying the relevance of each document cited in the IDS to the claimed invention. However, it is clear from this statute that such an explanation is required only for information listed that is not in English (37 C.F.R. 1.98(a)(3)(i)):

A concise explanation of the relevance ...of each patent, publication or other information listed **that is not in the English language**. The concise explanation may be either separate from applicant's specification or incorporated therein.

Therefore, Applicants are not required to provide a concise application for any of the references cited in the IDS. Certainly, the Examiner must consider the IDS filed June 28, 2005, which contains only 8 references.

In sum, the documents submitted in the Information Disclosure Statements in this application should all be considered on their merits.

Inventorship

After the mailing of this Office Action (*i.e.*, on June 28, 2005), Applicants filed a Petition to Correct Inventorship and accompanying documents. Applicants request acknowledgment that the change in inventorship has been entered.

35 U.S.C. § 112, 1st Paragraph, Written Description

Previous claims 38, 39, and 45 were rejected under 35 U.S.C § 112, first paragraph as allegedly not described by the specification as filed. (Office Action, pages 2-5). In particular, it was asserted that the written description requirement was not satisfied because the claims did not limit the polynucleotide sequence to any particular length. *Id.*

By amendment herein, Applicants have amended the claims as shown above to specify that the sequences of the claimed expression cassettes much exhibit at least 90% identity to the full-length of the recited sequences (identified by SEQ ID NO). Thus, the rejection has been obviated.

CONCLUSION

In view of the foregoing amendments and remarks, Applicants submit that the claims are now in condition for allowance and request early notification to that effect.

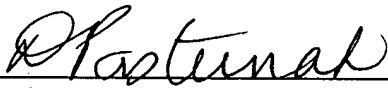
Please direct all further written communications regarding this application to:

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Respectfully submitted,

Date: August 30, 2005

By: _____



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ClustalW Results

Results of search	
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Sequence type	nt
ClustalW version	1.82
JalView	
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Guide tree file	clustalw-20050726-22511744.dnd
Your input file	clustalw-20050726-22511744.input
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To save a result file right-click the file link in the above table and choose "Save link as..."
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1 seqid46	97	8 seqid124	2529	97

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PLEASE NOTE: Some scores may be missing from the above table if the alignment output.

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Alignment

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CLUSTAL W (1.82) multiple sequence alignment

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seqid132      AAGCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCC
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seqid124      AAGCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCC
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seqid127      AAGCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCC
seqid46      -----
seqid47      -----
seqid125      AAGCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCC
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seqid47      -----
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seqid127      GTGGAGATCAACTGCACCCGCCCCAACAACAACACCCGCAAGAGCC
seqid46      -----
seqid47      -----
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seqid47      -----
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seqid47      -----
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seqid46      -----
seqid47      -----
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seqid47      -----
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seqid47      -----
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seqid47      -----
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seqid47      -----
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seqid132 GATCAGCAACTACACCGGCCTGATCTACAACCTGCTGGAGGACAGC
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seqid123 GATCAGCAACTACACCGGCCTGATCTACAACCTGCTGGAGGACAGC
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seqid127 GATCAGCAACTACACCGGCCTGATCTACAACCTGCTGGAGGACAGC
seqid46 -----
seqid47 -----
seqid125 GATCAGCAACTACACCGGCCTGATCTACAACCTGCTGGAGGACAGC
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seqid127 GAAGAACGAGAAGGACCTGCTGGAGCTGGACAAGTGAACAACCTC
seqid46 -----
seqid47 -----
seqid125 GAAGAACGAGAAGGACCTGCTGGAGCTGGACAAGTGAACAACCTC
seqid131 GAAGAACGAGAAGGACCTGCTGGAGCTGGACAAGTGAACAACCTC
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seqid126 CATCAGCAACTGGCCCTGGTACATCAAGATCTTCATCATGATCGTC
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seqid46 -----
seqid47 -----
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seqid131      CATCAGCAACTGGCCCTGGTACATCTAA-----

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seqid47      -----
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seqid121      -----
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seqid125      CCTGAGCTTCCAGACCCTGACCCCCAGCCCCGCGGCCTGGACCG(
seqid131      -----

seqid119      -----
seqid120      -----
seqid121      -----
seqid132      -----
seqid133      -----
seqid122      GGAGGAGGGCGGCGAGCAGGACCGCGACCGCAGCATCCGCCTGGTC
seqid123      GGAGGAGGGCGGCGAGCAGGACCGCGACCGCAGCATCCGCCTGGTC
seqid124      GGAGGAGGGCGGCGAGCAGGACCGCGACCGCAGCATCCGCCTGGTC
seqid126      GGAGGAGGGCGGCGAGCAGGACCGCGACCGCAGCATCCGCCTGGTC
seqid127      GGAGGAGGGCGGCGAGCAGGACCGCGACCGCAGCATCCGCCTGGTC
seqid46      -----
seqid47      -----
seqid125      GGAGGAGGGCGGCGAGCAGGACCGCGACCGCAGCATCCGCCTGGTC
seqid131      -----

seqid119      -----
seqid120      -----
seqid121      -----
seqid132      -----
seqid133      -----
seqid122      CCTGGCCTGGGACGACCTGCGCAACCTGTGCCTGTTTCAGCTACCA(
seqid123      CCTGGCCTGGGACGACCTGCGCAACCTGTGCCTGTTTCAGCTACCA(
seqid124      CCTGGCCTGGGACGACCTGCGCAACCTGTGCCTGTTTCAGCTACCA(
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seqid126      CCTGGCCTGGGACGACCTGCGCAACCTGTGCCTGTTTCAGCTACCA(
seqid127      CCTGGCCTGGGACGACCTGCGCAACCTGTGCCTGTTTCAGCTACCA(
seqid46      -----
seqid47      -----
seqid125      CCTGGCCTGGGACGACCTGCGCAACCTGTGCCTGTTTCAGCTACCA(
seqid131      -----

seqid119      -----
seqid120      -----
seqid121      -----
seqid132      -----
seqid133      -----
seqid122      CATCCTGATCGCCGTGCGCGCCGTGGAGCTGCTGGGCCACAGCAG(
seqid123      CATCCTGATCGCCGTGCGCGCCGTGGAGCTGCTGGGCCACAGCAG(
seqid124      CATCCTGATCGCCGTGCGCGCCGTGGAGCTGCTGGGCCACAGCAG(
seqid126      CATCCTGATCGCCGTGCGCGCCGTGGAGCTGCTGGGCCACAGCAG(
seqid127      CATCCTGATCGCCGTGCGCGCCGTGGAGCTGCTGGGCCACAGCAG(
seqid46      -----
seqid47      -----
seqid125      CATCCTGATCGCCGTGCGCGCCGTGGAGCTGCTGGGCCACAGCAG(
seqid131      -----

seqid119      -----
seqid120      -----
seqid121      -----
seqid132      -----
seqid133      -----
seqid122      GCGCGGCTGGGAGATCCTGAAGTACCTGGGCAGCCTGGTGCAGTA(
seqid123      GCGCGGCTGGGAGATCCTGAAGTACCTGGGCAGCCTGGTGCAGTA(
seqid124      GCGCGGCTGGGAGATCCTGAAGTACCTGGGCAGCCTGGTGCAGTA(
seqid126      GCGCGGCTGGGAGATCCTGAAGTACCTGGGCAGCCTGGTGCAGTA(
seqid127      GCGCGGCTGGGAGATCCTGAAGTACCTGGGCAGCCTGGTGCAGTA(
seqid46      -----
seqid47      -----
seqid125      GCGCGGCTGGGAGATCCTGAAGTACCTGGGCAGCCTGGTGCAGTA(
seqid131      -----

seqid119      -----
seqid120      -----
seqid121      -----
seqid132      -----
seqid133      -----
seqid122      GAAGAAGAGCGCCATCAGCCTGCTGGACACCATCGCCATCACCGT(
seqid123      GAAGAAGAGCGCCATCAGCCTGCTGGACACCATCGCCATCACCGT(
seqid124      GAAGAAGAGCGCCATCAGCCTGCTGGACACCATCGCCATCACCGT(
seqid126      GAAGAAGAGCGCCATCAGCCTGCTGGACACCATCGCCATCACCGT(
seqid127      GAAGAAGAGCGCCATCAGCCTGCTGGACACCATCGCCATCACCGT(
seqid46      -----
seqid47      -----
seqid125      GAAGAAGAGCGCCATCAGCCTGCTGGACACCATCGCCATCACCGT(
seqid131      -----

seqid119      -----
seqid120      -----
seqid121      -----
seqid132      -----
```

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seqid133 -----
seqid122 CCGCATCATCGAGCTGGTGCAGCGCATCTGCCGCGCCATCCTGAA(
seqid123 CCGCATCATCGAGCTGGTGCAGCGCATCTGCCGCGCCATCCTGAA(
seqid124 CCGCATCATCGAGCTGGTGCAGCGCATCTGCCGCGCCATCCTGAA(
seqid126 CCGCATCATCGAGCTGGTGCAGCGCATCTGCCGCGCCATCCTGAA(
seqid127 CCGCATCATCGAGCTGGTGCAGCGCATCTGCCGCGCCATCCTGAA(
seqid46 -----
seqid47 -----
seqid125 CCGCATCATCGAGCTGGTGCAGCGCATCTGCCGCGCCATCCTGAA(
seqid131 -----

```

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seqid119 -----
seqid120 -----
seqid121 -----
seqid132 -----
seqid133 -----
seqid122 CCGCCAGGGCTTCGAGGCCGCCCTGCTGTAACCTCGAG 2397
seqid123 CCGCCAGGGCTTCGAGGCCGCCCTGCTGTAACCTCGAG 2529
seqid124 CCGCCAGGGCTTCGAGGCCGCCCTGCTGTAACCTCGAG 2529
seqid126 CCGCCAGGGCTTCGAGGCCGCCCTGCTGTAACCTCGAG 2616
seqid127 CCGCCAGGGCTTCGAGGCCGCCCTGCTGTAACCTCGAG 2616
seqid46 -----
seqid47 -----
seqid125 CCGCCAGGGCTTCGAGGCCGCCCTGCTGTAACCTCGAG 2613
seqid131 -----

```

PLEASE NOTE: Showing colors on large alignments is slow.

Show Colors

View Alignment File

Guide Tree

Show as Phylogram Tree

Show Distances

View DND F

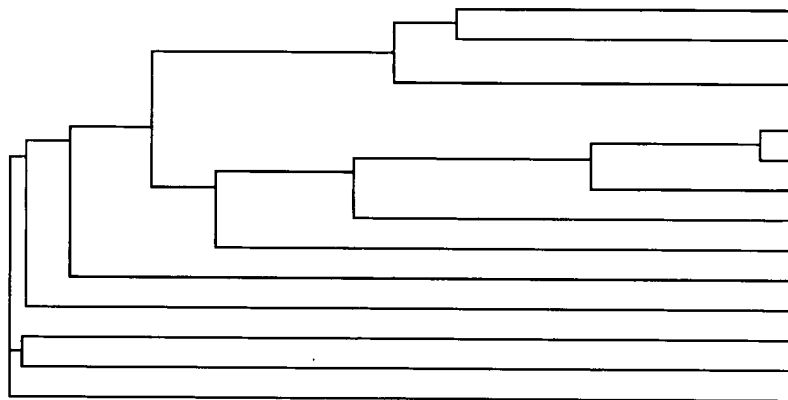
```

(
(
(
(
(
(
seqid46:-0.00705,
seqid47:0.00705)
:0.00360,
(
seqid125:-0.00719,
seqid131:0.00817)
:0.02358)
:0.01417,
(
(
(
(
(

```

```
seqid122:0.01713,  
seqid123:-0.01713)  
:0.00978,  
seqid124:-0.00734)  
:0.01374,  
seqid126:-0.01249)  
:0.00803,  
seqid127:-0.00255)  
:0.00380)  
:0.00475,  
seqid133:0.00545)  
:0.00253,  
seqid132:0.00078)  
:0.00102,  
(  
seqid119:0.00677,  
seqid120:-0.00066)  
:0.00081,  
seqid121:0.00274);
```

Cladogram



☐ Show as Phylogram Tree ☐ Show Distances ☐ View DND F

*Right-click on the above tree to see display options.
Problems printing? Read [how to print a Phylogram or Cladogram](#).*

CLUSTAL W (1.82) multiple sequence alignment

```

seqidno120      GAATTCATGCGCGTGATGGGCACCCAGAAGAACTGCCAGCAGTGGTGGATCTGGGGCATC 60
seqidno121      GAATTCATGCGCGTGATGGGCACCCAGAAGAACTGCCAGCAGTGGTGGATCTGGGGCATC 60
*****

seqidno120      CTGGGCTTCTGGATGCTGATGATCTGCAACACCGAGGACCTGTGGGTGACCGTGACTAC 120
seqidno121      CTGGGCTTCTGGATGCTGATGATCTGCAACACCGAGGACCTGTGGGTGACCGTGACTAC 120
*****

seqidno120      GGCCTGCCCCGTGTGGCGCGACGCCAAGACCACCCTGTTCTGCGCCAGCGACGCCAAGGCC 180
seqidno121      GGCCTGCCCCGTGTGGCGCGACGCCAAGACCACCCTGTTCTGCGCCAGCGACGCCAAGGCC 180
*****

seqidno120      TACGAGACCGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCACCGACCCCAAC 240
seqidno121      TACGAGACCGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCACCGACCCCAAC 240
*****

seqidno120      CCCAGGAGATCGTGCTGGGCAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATG 300
seqidno121      CCCAGGAGATCGTGCTGGGCAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATG 300
*****

seqidno120      GCCGACCAGATGCACGAGGACGTGATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTG 360
seqidno121      GCCGACCAGATGCACGAGGACGTGATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTG 360
*****

seqidno120      AAGCTGACCCCCCTGTGCGTGACCCTGAACTGCACCGACACCAACGTGACCGGCAACCGC 420
seqidno121      AAGCTGACCCCCCTGTGCGTGACCCTGAACTGCACCGACACCAACGTGACCGGCAACCGC 420
*****

seqidno120      ACCGTGACCGGCAACAGCACCAACAACACCAACGGCACCGGCATCTACAACATCGAGGAG 480
seqidno121      ACCGTGACCGGCAACAGCACCAACAACACCAACGGCACCGGCATCTACAACATCGAGGAG 480
*****

seqidno120      ATGAAGAACTGCAGCTTCAACGCCGGCGCCGGCCGCCTGATCAACTGCAACACCAGCACC 540
seqidno121      ATGAAGAACTGCAGCTTCAACGCCGGCGCCGGCCGCCTGATCAACTGCAACACCAGCACC 540
*****

seqidno120      ATCACCCAGGCCTGCCCAAGGTGAGCTTCGACCCCATCCCATCCACTACTGCGCCCCC 600
seqidno121      ATCACCCAGGCCTGCCCAAGGTGAGCTTCGACCCCATCCCATCCACTACTGCGCCCCC 600
*****

seqidno120      GCCGGCTACGCCATCCTGAAGTGCAACAACAAGACCTTCAACGGCACCGGCCCTGCTAC 660
seqidno121      GCCGGCTACGCCATCCTGAAGTGCAACAACAAGACCTTCAACGGCACCGGCCCTGCTAC 660
*****

seqidno120      AACGTGAGCACCGTGCACTGCACCCACGGCATCAAGCCCGTGGTGAGCACCCAGCTGCTG 720
seqidno121      AACGTGAGCACCGTGCACTGCACCCACGGCATCAAGCCCGTGGTGAGCACCCAGCTGCTG 720
*****

seqidno120      CTGAACGGCAGCCTGGCCGAGGAGGGCATCATCATCCGCAGCGAGAACCTGACCGAGAAC 780
seqidno121      CTGAACGGCAGCCTGGCCGAGGAGGGCATCATCATCCGCAGCGAGAACCTGACCGAGAAC 780
*****

seqidno120      ACCAAGACCATCATCGTGCACCTGAACGAGAGCGTGGAGATCAACTGCACCCGCCCCAAC 840
seqidno121      ACCAAGACCATCATCGTGCACCTGAACGAGAGCGTGGAGATCAACTGCACCCGCCCCAAC 840
*****

seqidno120      AACAACACCCGCAAGAGCGTGCGCATCGGCCCCGGCCAGGCCTTCTACGCCACCAACGAC 900

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seqidno121  AACAACACCCGCAAGAGCGTGCGCATCGGCCCCGGCCAGGCCTTCTACGCCACCAACGAC  900
*****

seqidno120  GTGATCGGCAACATCCGCCAGGCCCCTGCAACATCAGCACCGACCGCTGGAACAAGACC  960
seqidno121  GTGATCGGCAACATCCGCCAGGCCCCTGCAACATCAGCACCGACCGCTGGAACAAGACC  960
*****

seqidno120  CTGCAGCAGGTGATGAAGAAGCTGGGCGAGCACTTCCCCAACAAGACCATCCAGTTCAAG  1020
seqidno121  CTGCAGCAGGTGATGAAGAAGCTGGGCGAGCACTTCCCCAACAAGACCATCCAGTTCAAG  1020
*****

seqidno120  CCCACGCCGGCGGCGACCTGGAGATCACCATGCACAGCTTCAACTGCCGCGGCGAGTTC  1080
seqidno121  CCCACGCCGGCGGCGACCTGGAGATCACCATGCACAGCTTCAACTGCCGCGGCGAGTTC  1080
*****

seqidno120  TTCTACTGCAACACCAGCAACCTGTTCAACAGCACCTACCACAGCAACAACGGCACCTAC  1140
seqidno121  TTCTACTGCAACACCAGCAACCTGTTCAACAGCACCTACCACAGCAACAACGGCACCTAC  1140
*****

seqidno120  AAGTACAACGGCAACAGCAGCAGCCCCATCACCCTGCAGTGCAAGATCAAGCAGATCGTG  1200
seqidno121  AAGTACAACGGCAACAGCAGCAGCCCCATCACCCTGCAGTGCAAGATCAAGCAGATCGTG  1200
*****

seqidno120  CGCATGTGGCAGGGCGTGGGCCAGGCCACCTACGCCCCCCCCATCGCCGGCAACATCACC  1260
seqidno121  CGCATGTGGCAGGGCGTGGGCCAGGCCACCTACGCCCCCCCCATCGCCGGCAACATCACC  1260
*****

seqidno120  TGCCGCAGCAACATCACCGGCATCCTGCTGACCCGCGACGGCGGCTTCAACACCACCAAC  1320
seqidno121  TGCCGCAGCAACATCACCGGCATCCTGCTGACCCGCGACGGCGGCTTCAACACCACCAAC  1320
*****

seqidno120  AACACCGAGACCTTCCGCCCCGGCGGCGGCGACATGCGCGACAACCTGGCGCAGCGAGCTG  1380
seqidno121  AACACCGAGACCTTCCGCCCCGGCGGCGGCGACATGCGCGACAACCTGGCGCAGCGAGCTG  1380
*****

seqidno120  TACAAGTACAAGGTGGTGGAGATCAAGCCCCTGGGCATCGCCCCCACCAGGCCAAGCGC  1440
seqidno121  TACAAGTACAAGGTGGTGGAGATCAAGCCCCTGGGCATCGCCCCCACCAGGCCATCAGC  1440
*****

seqidno120  CGCGTGGTGCAGCGCGAGAAGCGCGCCGTGGGCATCGGCGCCGTGTTCTGGGCTTCCTG  1500
seqidno121  AGCGTGGTGCAGAGCGAGAAGAGCGCCGTGGGCATCGGCGCCGTGTTCTGGGCTTCCTG  1500
*****

seqidno120  GGCGCCCGGGCAGCACCATGGGCGCCGCCAGCATCACCTGACCGTGCAGGCCCGCCAG  1560
seqidno121  GGCGCCCGGGCAGCACCATGGGCGCCGCCAGCATCACCTGACCGTGCAGGCCCGCCAG  1560
*****

seqidno120  CTGCTGAGCGGCATCGTGCAGCAGCAGAGCAACCTGCTGAAGGCCATCGAGGCCCAGCAG  1620
seqidno121  CTGCTGAGCGGCATCGTGCAGCAGCAGAGCAACCTGCTGAAGGCCATCGAGGCCCAGCAG  1620
*****

seqidno120  CACATGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGTGGCCATC  1680
seqidno121  CACATGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGTGGCCATC  1680
*****

seqidno120  GAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCCGCTGATC  1740
seqidno121  GAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCCGCTGATC  1740
*****

seqidno120  TGCACCACCGCCGTGCCCTGGAACAGCAGCTGGAGCAACAAGAGCGAGAAGGACATCTGG  1800

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seqidno121      TGCACCACCGCCGTGCCCTGGAACAGCAGCTGGAGCAACAAGAGCGAGAAGGACATCTGG 1800
*****

seqidno120      GACAACATGACCTGGATGCAGTGGGACCGCGAGATCAGCAACTACACCGGCCTGATCTAC 1860
seqidno121      GACAACATGACCTGGATGCAGTGGGACCGCGAGATCAGCAACTACACCGGCCTGATCTAC 1860
*****

seqidno120      AACCTGCTGGAGGACAGCCAGAACCAGCAGGAGAAGAACGAGAAGGACCTGCTGGAGCTG 1920
seqidno121      AACCTGCTGGAGGACAGCCAGAACCAGCAGGAGAAGAACGAGAAGGACCTGCTGGAGCTG 1920
*****

seqidno120      GACAAGTGGAAACAACCTGTGGAAC TGGTTCGACATCAGCAACTGGCCCTGGTACATCTAA 1980
seqidno121      GACAAGTGGAAACAACCTGTGGAAC TGGTTCGACATCAGCAACTGGCCCTGGTACATCTAA 1980
*****

seqidno120      CTCGAG 1986
seqidno121      CTCGAG 1986
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